

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 12:13:05 : Search time 5703.43 Seconds
(without alignments)
18957.079 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169

Sequence: 1 acctgtgtcagttaccctc.....cttggtccctccatgtcag 6169

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 17159718 seqs, 8763200856 residues

Total number of hits satisfying chosen parameters: 34319436

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6169	100.0	6169	13	US-08-938-669-3	Sequence 3, App11
2	6169	100.0	6169	16	US-09-227-881-3	Sequence 3, App11
3	6169	100.0	6169	17	US-09-306-828-1	Sequence 3, App11
4	5594.8	90.7	7360	50	US-60-172-360-23866	Sequence 23866, A
5	5275.4	85.5	5300	13	US-08-938-669-1	Sequence 1, App11
6	5275.4	85.5	5300	16	US-09-227-881-1	Sequence 1, App11
7	5275.4	85.5	5300	17	US-09-306-828-1	Sequence 1, App11
8	5271	85.4	5271	16	US-09-227-881-34	Sequence 34, App1
9	5271	85.4	5271	13	US-08-938-669-2	Sequence 2, App11
10	5253.4	85.2	5304	16	US-09-227-881-2	Sequence 2, App11
11	5253.4	85.2	5304	17	US-09-306-828-2	Sequence 2, App11
12	5253.4	85.2	5304	17	US-09-306-828-2	Sequence 2, App11
13	2677.4	43.4	2800	14	US-09-056-285-1	Sequence 1, App11
14	2677.4	43.4	2800	17	US-09-306-828-26	Sequence 26, App1
15	2677.4	43.4	2800	17	US-09-306-828-26	Sequence 26, App1
16	2480.8	40.2	2666	11	US-08-791-154-3	Sequence 3, App11
17	2238.2	36.3	2397	11	US-08-791-154-1	Sequence 1, App11
18	1821.6	29.5	1950	11	US-08-791-154-2	Sequence 2, App11
19	640.4	10.4	1548	13	US-08-938-669-26	Sequence 26, App1
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21	640.4	10.4	1548	17	US-09-306-828-26	Sequence 26, App1
22	640.4	10.4	1871	19	US-09-509-516-1	Sequence 1, App11
23	640.4	10.4	1871	19	US-09-509-516-18	Sequence 18, App1
24	640.4	10.4	1999	10	US-08-667-790-2	Sequence 2, App11
25	640.4	10.4	1999	26	US-09-666-547-2	Sequence 2, App11
26	614.2	10.0	2181	65	US-60-324-185-14659	Sequence 14659, A
27	604.4	9.8	1512	10	US-08-667-790-3	Sequence 3, App11
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29	604.4	9.8	1515	14	US-09-056-285-7	Sequence 7, App11
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35	556.6	9.0	1969	9	US-08-546-568-2	Sequence 2, App11
36	556.6	9.0	1969	12	US-08-882-238-2	Sequence 2, App11
37	556.6	9.0	1969	12	US-08-882-238-2	Sequence 2, App11
38	519.6	8.4	1491	9	US-08-546-568-3	Sequence 3, App11
39	519.6	8.4	1491	9	US-08-546-568-3	Sequence 3, App11
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41	494.4	8.0	503	19	US-09-528-409-110729	Sequence 110729, A

42	494.4	8.0	503	32	US-09-933-524-110729	Sequence 110729,
43	427	6.9	716	51	US-60-188-162-343	Sequence 343, App
44	388.2	6.3	413	16	US-09-293-972-32481	Sequence 32481, A
45	382.8	6.2	1473	14	US-09-056-285-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-08-938-669-3

; Sequence 3, Application US/08938669

; GENERAL INFORMATION:

; APPLICANT: Nguyen, Thai D.

; APPLICANT: Polansky, Jon R.

; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,

; TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND RELATED DISEASE

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howrey & Simon

; STREET: 1299 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004-2402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/938,669

; FILING DATE:

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/791,154

; FILING DATE: 28-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Sila, Serge

; REGISTRATION NUMBER: 39,445

; REFERENCE/DOCKET NUMBER: 07425-0034

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 383-6857

; TELEFAX: 202 383-6610

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6169 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-938-669-3

; Query Match

; Best local Similarity 100.0%; Score 6169; DB 13; Length 6169;

; Matches 6169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	241	catcaaacaggaactgaagaacgaatgaatgagacacttgcacgaagaataatccag	300
DB	241	CATCAACAGGAGCTAAGAACAGAAATGATGGACCTTGCCAAAGGAATAATCCAG	300
QY	301	gagagcaaatatgaatgaataataacttcccttgttctttaatctcaggaataatg	360
DB	301	GAGAGCAAAATATGATGAATAATAACTTTCCCTTGTGTTTAAATTCAGGAATAATG	360
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DB	841	GGGAGCCCTGAGCATTTGCCCTTAGGAAAGCCAGTTTCTTAAGGAATCTTAAGAAATCTC	900
QY	901	ctgaagaatcagaatcttaacacatttaagataaacaataatgcatgataatcag	960
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QY	961	cttaagacatgggtcccaattttaaaagtcagacataagaataaagctgtccacgtcc	1020
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Db	3301	ggtagccttctgcctgcgtcatccaataacttgggcagaagcagaagtgaanaaigtccacagaatlg	3360
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RESULT      2
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: Sequence 3, Application US/09227881
: GENERAL INFORMATION:
:   APPLICANT: Nguyen, Thai D.
:   APPLICANT: Polansky, Jon R.
:   APPLICANT: Chen, Pu
:   APPLICANT: Chen, Hua
:   TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
:   CURRENT APPLICATION NUMBER: US/09/227,881
:   CURRENT FILING DATE: 1999-01-11
:   EARLIER APPLICATION NUMBER: US 08/938,669
:   EARLIER FILING DATE: 1997-09-26
:   NUMBER OF SEQ ID NOS: 36
:   SOFTWARE: Microsoft word 97
:   SEQ ID NO 3
:   LENGTH: 6169
:   TYPE: DNA
:   ORGANISM: Homo sapiens
US-09-227-881-3

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Query Match	100.0%	Score 6169;	DB 16;	Length 6169;
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; GENERAL INFORMATION:
; APPLICANT: Nuyven, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; NUMBER OF SEQ ID NOS: 38
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; LENGTH: 6169
; TYPE: DNA
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RESULT 4
US-60-172-360-23886
; Sequence 23886, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diop, Din
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GA-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; NUMBER OF FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 23838
; SOFTWARE: PERL Program
; SEQ ID NO 23886
; LENGTH: 7369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 223079.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1321-1562, 4158-4182, 4874-4912, 4986-5023
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-360-23886

Query Match 90.7% Score 5594.8; DB 50; Length 7369;
Best Local Similarity 94.2% Pred. No. 0;
Matches 5596; Conservative 0; Mismatches 346; Indels 0; Gaps 0;

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Oy 61 tccataaacgtatagcctcattcgatgtatgtcttggcagagatgaagaatca 120

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Qy	1441	gttcaacacatataagccggtgtctctgaactccctgaactcagatgaatccaccactc	1500
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Db	781	gacatggtgttaaaagcagaccagaaacattgtagccttcaagaaagagagccctccagca	840
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QY	901	ttgaaagaatcatatgtaattttaacattttaagtaataaacaatatgucgattgataatcag	960
Db	901	ttgaaagaatcatatgtaattttaacattttaagtaataaacaatatgucgattgataatcag	960
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Db	961	tttagacaattggtgcccaattttaaaagtacagcatacaagaataaagttcccgctcc	1020
QY	1021	ggataagtcagaaatcatcttagaaatcaactgtgtccccaactcttaacttttcagaaatgac	1080
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QY	1081	tgataagccttcacacagagcccgatgtgtctgagcctacagaaacatcttcaacccaa	1140
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QY	1201	tgtgcagccaatcccgctccacagagaagttccccaactttagactctgcatacagatgt	1260
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[illegible]

[illegible][illegible]

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RESULT      9
US-09-306-828-34
; Sequence 34, Application US/09306828
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-34

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Query Match	85.48; Score 5271; DB 17; Length 5271;
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[illegible]

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RESULT 11
US-09-227-881-2
: Sequence 2, Application US/09227881
: GENERAL INFORMATION:
: APPLICANT: Nguyen, Thai D.
: APPLICANT: Polansky, Jon R.
: APPLICANT: Chen, Pu
: APPLICANT: Chen, Hua
: TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
: CURRENT APPLICATION NUMBER: US/09/227,881
: CURRENT FILING DATE: 1999-01-11
: EARLIER APPLICATION NUMBER: US 08/938,669
: EARLIER FILING DATE: 1997-09-26
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: Microsoft Word 97
: SEQ ID NO 2
: LENGTH: 5304
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-227-881-2

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Query Match	85.28;	Score	5253.4;	DB	16;	Length	5304;	
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Matches 5993;	Conservative	0;	Mismatches	6;	Indels	6;	Gaps	3

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RESULT      12
US-09-306-828-2
: Sequence 2: Application US/09306828
: GENERAL INFORMATION:
: APPLICANT: Nguyen, Thai D.
: APPLICANT: Polansky, Jon R.
: APPLICANT: Chen, Pu
: TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
: CURRENT APPLICATION NUMBER: US/09/306,828
: CURRENT FILING DATE: 1999-05-07
: EARLIER APPLICATION NUMBER: US 09/227,881
: EARLIER FILING DATE: 1999-01-11
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Microsoft Word 97
: SEQ ID NO 2
: LENGTH: 5304
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-306-828-2

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RESULT 14

US-09-056-285A-1

Sequence 1, Application US/09056285A

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.

Sheffield, Val C.

Alward, Wallace L.M.

Fingerl, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESS: FOLEY, HONG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056, 285A

FILING DATE: 07-Apr-1998

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: UIA-010, 28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2800 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-056-285A-1

Query Match 43.4%; Score 2677.4; DB 14; Length 2800;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2736; Conservative 0; Mismatches 1; Indels 8; Gaps 5;

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Db 659 GCAATCATTAATTAAGGCGCTTAAAGTTACTTCTGACAGTTTGGTAATTAATTTGGCT 718
OY 4150 attgcaatctgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 4209
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Db 719 ATTGCCATTTCCTTTTGTCTTTTCTCTTTGGTTTATTAATGTAAGCAAGCAAGATTATTA 778
OY 4210 accctacgtccagaagcctgtgaaattgaaatgagaanaaaatctacatttcttctac 4269
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Db 779 ACTTACAGTCCAGAAAGCGCTGTAATTTGANTGAGAAAAAATTAATTTTGTATTAC 838
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OY 4390 attacagttctgtagatagctgtglaagtgaataatctatactcaaaactacttgaat 4449
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Db 1199 ACACAGAGTAAAGAACTGATTAGAGGCTTAACATTTGACATTGTGCTGAGATGCAAGACT 1258
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[illegible]

QY	5890	gtctccagaccgagagacacgctctgggcgctggtccaccaggtctccagagaagtaagatg	5943
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Db	2699	tcaatttaagattagtggtttcagagattctctgtgtccctcccatgtcag	2743

RESULT 15
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Query Match 43.48; Score 2677.4; DB 17; Length 2800;

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Best local similarity 95.76; Prev. NO. 0;
Matches 2736; Conservative 0; Mismatches 1; Indels 8; Gaps 5;

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QY 3431 agccagcaggggaggaagaagaaggaggatggtatgagccaagaagaacagatctcat 3490

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QY 3491 tcaaggcagatgaggaaattgaccacagggattatagtcacgtgtaactcgtggtcttagag 3550

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Oy	3551	gcaagggtacatctgtcggygggaaaaaaatcagltccaaaggaagtcggyagacctgaattct	3610
Db	120	GCAGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGAGACCTGATTTCT	179
Oy	3611	aatctataatttctcttctcaagctgagtaattctgagcaagtcagaagtagtaactg	3670
Db	180	AATACATATATTTTTCCTTTCAAGCGTAGAATTTTGACAGCAAGTACAGAGTAACTG	239
Oy	3671	aggtctgaagaataactagtaatttctcttataggaactctttctctgtagagtaaga	3730
Db	240	AGGCTGTAAAGATTATCTTAAGTTCTCCTATTATAGGAACCTTTTTCCTGTGGAGTTTACA	299
Oy	3731	gcacaagggaatcccgctctcttcttaacaggaagaaacatctcctaagtaagaaccaa	3790
Db	300	GCACAAAGGCAATCCGTTTCTTTAAAGGAAGAAACATTTCTAAGAGTAAACCCAA	359
Oy	3791	cagatccaagccttagtctgtcgtactataatgattggtttttgaaaaatcattcagcg	3850
Db	360	CAGATTCACAGCTTAGCTCTGCTGACTAATATGATTTGGTTTTGAAAAATCTTTCACGC	419
Oy	3851	atgtttctactcttgatctcagaaaaatgaagctagaccctttgtaagctgttaaaaaa	3910
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Oy	3911	cccaagctgataaagtcctcgaagctcgaagcttaactgacagaaacatacaa-aagaaaga	3969
Db	480	CCCATTTGTAAATGTCCTCAAGTTCCAGCTTAAGTGCAGAACCAATCAATTAAGATTA	539
Oy	3970	tctttagagcaaacgtgttcttctccacatctggaagtgaagtcgtccagggcagtttgaa	4039
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Oy	4030	atatttctctcaagaatctgaacaagctgtgtgatacttaacaacaataagttgtccaag	4089
Db	599	ATATTACTTTCACAGATTAATGGACATGTTGTGGTATTAACAACAATAAATGGTCTCAAG	658
Oy	4090	gcaatcaatattcgaagtgcctcgaagtaactctgaacgtcttgataattatctgtct	4149
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Oy	4150	atgcaatctgtcttctgttttctctcttctggtttatataagtaagcaggaattata	4209
Db	719	ATTGCGCATTTGCTTTTGTTTTCTTCTTGGGTATTAATGTAAGACGAGATTATTA	778
Oy	4210	acctcaagtcagaagaagccgtgtaattgaaagaaaaaaataacatttctgttctaac	4265
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Db	899	GTAATTAACAGTACCTGATTTTGTCAATTACCAATGAAATCAAGACATTTTATATCAT	958
Oy	4380	atcaagctgtctgacgaataagctgtgaagaaatattatactcaaaactacttgaat	4449
Db	959	ATTACAGTTGTGCAAGTATAGCTGTGAAGCAAAATTTTATCTCAAAACTACTTTGGAAT	1018
Oy	4450	taagaccctgcgcgacatctgtcttcttaacataataaacaatcttaaaatttgata	4509
Db	1019	TAGACCTCTGCTGATCTTGTTTTAACTATTAATTAACATGTTTTAAATTTTGATA	1078
Oy	4510	tcttgataatacataattcatatcaatctgttctctctgtaactataattataatctg	4569
Db	1079	TTTTGATTAATCATATTTTCATTATCATTTATTTGTTTCTTGTGAATCTATATTTATATTTG	1138
Oy	4570	aaaaacatcttctgagaagaagctccccaagattcaccaatlgaggttcttggaagcac	4629
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OY	4990	gtgtacgt	5049
Db	1559	GTTGATACGT	1618
OY	5050	ctattgggggtatgggtgacataaatttgagbatgtctttttaaagaabccccaagaagac	5109
Db	1619	TTATTTGGGGGTATGGGTGCTCATTAATTTGGAGATGTTCTTTTAAAAACCAACTCCAAACAGAC	1678
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OY	5170	agccccaaccagccctcaagctgagccacctgtctcttcccatagaaggctgtgtccccag	5229
Db	1739	AGCCCAACCCAGCTTCAGTGGGACCTGCTGTCTTCCCAATGAAGGGCTGGCTGCCAG	1798
OY	5230	tatatataaacctctctcgtgagcttcgggcaatgagcagaagccacccaatccatccagacct	5289
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OY	5290	ctcagcaacagagagctcttcacagaaggagccctacaacaaacccctgtcaatlgaggtctctc	5349
Db	1859	CTCAGCAACAGAGAGCTTTCAGAGGGAAGCTTCACCAACGCTCTGCATMGAGGTTCTTCT	1918
OY	5350	gttgcacgttctgcagctcttgggacctgagatgcccagctgtctcagctgtcgtctctgtacct	5409
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OY	5470	gcccagatgccaatgatacctctcagttgtgtgccaagtcaccaatgaatcagctgtgccagaagcaga	5529
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Db	2099	GCCAGGCCATCTCATGATCATTAACCTTACAGAGGAACAGCAACCCACAGCTTGAAGCC	2158
OY	5590	tggaaggccaacaaagctcgaactcagctctccctggaaggccctctccacaacatlgagacctgtg	5649
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OY	5650	accagagctgcaggccccaaggaagaccagaaggagctgcagaaggagcttggagccactga	5709
Db	2219	ACCAAGGCTGCCAGGCCCCAGAGAACCCAGAGGGGCTTGAGAGGGAGAGCTTGGGCAACCTGGA	2278

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QY 5710 ggcgggagcggggaccagcttgaaacccaacagagatgttgagactgcttacaacaac 5769
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QY 5770 tcctccgagacaagtcagctctgagagagagaaagcgactaaggcaagaaatgaga 5829
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QY 6066 aactaaagaaagaca-cgaatcaccttcaagtaactaagtaattagctcctgaagct 6124
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Db 2639 AATTAAAGAAAGCACAGCGATCACTTCAAGTATTAATAATTAGTCTCTGAGAGCT 2698
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QY 6125 tcaattagaltagtggttcagagctctctgtgcccctccatgctcag 6169
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Db 2699 TCATTAGATTAGTGTGCTCAGAGTCTGTGTGCCCTGCATGCTCAG 2743
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 Job time: 40797 sec